



SEQUENCE LISTING

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OCT 22 2001
TECH CENTER 1600/2900

<110> MCGILL UNIVERSITY
SZYF, Moshe
BHATTACHARYA, Sanjoy K.
RAMCHANDANI, Shyam

<120> DNA DEMETHYLASE, THERAPEUTIC AND
DIAGNOSTIC USES THEREOF

<130> 1770-183"PCT" FC/ld

<150> CA 2,220,805

<151> 1997-11-12

<150> CA 2,230,991

<151> 1998-05-11

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1804

<212> DNA

<213> Unknown

<220>

<223> cDNA encoding human demethylase

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aacctcagct ggcaagatac ctgggaaatg ctggtgacct tagcagtttt gacttcagga 720
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1740
 1800
 1804

<210> 2
 <211> 411
 <212> PRT
 <213> Unknown

<220>
 <223> predicted amino acid of human demethylase

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 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
 35 40 45
 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335
 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365
 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
 370 375 380

Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
 385 390 395 400
 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
 405 410

<210> 3
 <211> 1589
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA sequence of human dMTase2

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 ggacagaaca gctgcggcga gtggcggcgg cggaggggagc cgaatcggcg acgagcccgg 180
 ggggtcgcaac ttgcagaagc ggcggcggcg gcggcatcgg ccacggcggg cggaaaagcc 240
 ggggcgcaat ggagcgggaag aggtgggagt gcccggcgct cccgcagggc tgggaaaggg 300
 aagaagtgc caggaggctg gggctgtcgg ccggccacag ggatgtcttt tactatagcc 360
 ccagcgggaa gaagtccgc agcaagccac aactggcacg ttacctgggc ggatccatgg 420
 acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc 480
 gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacaccg 540
 cgctgcctgt acggcagact gcatccatct tcaagcaacc ggtgaccaag atcaccaacc 600
 accccagcaa caaggtcaag agcgacccgc agaaggcagt ggaccagccg aggcagcttt 660
 tctgggagaa gaagctaagt ggattgagt cctttgacat tgcagaagaa ctggtcagga 720
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 tgtcagccat tgcgagtgt ctacacacca gcaccctgcc cattacaggc cagctctctg 840
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<210> 4
 <211> 291
 <212> PRT
 <213> Unknown

<220>
 <223> predicted amino acid sequence of human dMTase2

<400> 4

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 20 25 30
 Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 35 40 45
 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
 50 55 60
 Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
 65 70 75 80

Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
 85 90 95
 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 100 105 110
 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 115 120 125
 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
 130 135 140
 Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
 145 150 155 160
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
 165 170 175
 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
 180 185 190
 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
 195 200 205
 Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
 210 215 220
 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
 225 230 235 240
 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
 245 250 255
 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
 260 265 270
 Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
 275 280 285
 Glu His Val
 290

<210> 5
 <211> 1966
 <212> DNA
 <213> Unknown

 <220>
 <223> cDNA sequence of mouse dMTase1

<400> 5
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 aagggtctcg ttacggaaga agcgcagcgc cggctgggga gggggctgga tgcgcgcgca 240
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tttttgatgt	atatatctat	tattcaaaaa	atcatgttta	ttttgagtcc	taggacttaa	1680
aattagtctt	ttgtaatatc	aagcaggacc	ctaagatgaa	gctgagcttt	tgatgccagg	1740
tgcaatctac	tggaatgta	gcacttacgt	aaaacatttg	tttccccac	agttttaata	1800
agaacagatc	aggaattcta	aataaatttc	ccagttaaag	attattgtga	cttcactgta	1860
tataaacata	tttttatact	ttattgaaag	gggacacctg	tacattcttc	catcatcact	1920
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<210> 6

<211> 414

<212> PRT

<213> Unknown

<220>

<223> predicted amino acid sequence of mouse dMTase1

<400> 6

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Glu	Gln	Gly	Gly	Gln	Gly	Ser	Ala	Leu	Ala	Pro	Ser	Pro	Val	Ser	Gly	
			35				40					45				
Val	Arg	Arg	Glu	Gly	Ala	Arg	Gly	Gly	Gly	Arg	Gly	Arg	Gly	Arg	Trp	
	50					55					60					
Lys	Gln	Ala	Ala	Arg	Gly	Gly	Gly	Val	Cys	Gly	Arg	Gly	Arg	Gly	Arg	
65					70				75					80		
Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	Gly	Arg	
				85				90						95		
Pro	Gln	Ser	Gly	Gly	Ser	Gly	Leu	Gly	Gly	Asp	Gly	Gly	Gly	Gly	Ala	
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Pro	Val	Pro	Phe	Pro	Ser	Gly	Ser	Ser	Gly	Pro	Gly	Pro	Arg	Gly	Pro	
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Lys	Ser	Asp	Val	Tyr	Tyr	Phe	Ser	Pro	Ser	Gly	Lys	Lys	Phe	Arg	Ser	
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Lys	Pro	Gln	Leu	Ala	Arg	Tyr	Leu	Gly	Asn	Ala	Val	Asp	Leu	Ser	Ser	
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Phe	Asp	Phe	Arg	Thr	Gly	Lys	Met	Met	Pro	Ser	Lys	Leu	Gln	Lys	Asn	
	210				215						220					
Lys	Gln	Arg	Leu	Arg	Asn	Asp	Pro	Leu	Asn	Gln	Asn	Lys	Gly	Lys	Pro	
225					230				235					240		
Asp	Leu	Asn	Thr	Thr	Leu	Pro	Ile	Arg	Gln	Thr	Ala	Ser	Ile	Phe	Lys	
				245					250					255		
Gln	Pro	Val	Thr	Lys	Phe	Thr	Asn	His	Pro	Ser	Asn	Lys	Val	Lys	Ser	
			260				265						270			
Asp	Pro	Gln	Arg	Met	Asn	Glu	Gln	Pro	Arg	Gln	Leu	Phe	Trp	Glu	Lys	
		275				280					285					
Arg	Leu	Gln	Gly	Leu	Ser	Ala	Ser	Asp	Val	Thr	Glu	Gln	Ile	Ile	Lys	
	290				295						300					
Thr	Met	Glu	Leu	Pro	Lys	Gly	Leu	Gln	Gly	Val	Gly	Pro	Gly	Ser	Asn	
305					310					315				320		
Asp	Glu	Thr	Leu	Leu	Ser	Ala	Val	Ala	Ser	Ala	Leu	His	Thr	Ser	Ser	

325	Ala Pro Ile Thr Gly Gln Val Ser	330	Ala Ala Val Glu Lys Asn Pro Ala
340	Val Trp Leu Asn Thr Ser Gln Pro	345	Leu Cys Lys Ala Phe Ile Val Thr
355	Asp Glu Asp Ile Arg Lys Gln Glu	360	Glu Arg Val Gln Gln Val Arg Lys
370	Lys Leu Glu Glu Ala Leu Met Ala	375	Asp Ile Leu Ser Arg Ala Ala Asp
385	Thr Glu Glu Val Asp Ile Asp Met	390	Asp Ser Gly Asp Glu Ala
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<210> 7
 <211> 2392
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA sequence of mouse dMTase2

<400> 7

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<210> 8
 <211> 285
 <212> PRT
 <213> Unknown

<220>

<223> predicted amino acid sequence of mouse dMTase2

<400> 8

Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
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 Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
 20 25 30
 Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 35 40 45
 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
 50 55 60
 Arg Thr Gly Lys Met Leu Met Asn Lys Met Asn Lys Ser Arg Gln Arg
 65 70 75 80
 Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
 85 90 95
 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 100 105 110
 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 115 120 125
 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
 130 135 140
 Gly Leu Ser Ala Phe Asp Ile Ala Glu Glu Leu Val Arg Thr Met Asp
 145 150 155 160
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
 165 170 175
 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Leu Pro Ile
 180 185 190
 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
 195 200 205
 Asn Thr Ala Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Asp Asp
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 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
 225 230 235 240
 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
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 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Glu Glu Glu Glu
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 of the putative demethylase candidate cDNA

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of the putative demethylase candidate cDNA

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